109.5 109.5 4.4 109.5	109.5 4 108.5 4 108 4	107	105.5 105.5 105.5 105.5	105.5	104.5 4	103.5 4	103.5	41 103.5 4.5 42 103.5 4.5 44 102.5 4.4	102.5	RESULT 1 090XY7 ID 090XY7 PRELIMI	DT 01-MAY-2000 (TYEMBL: DT 01-MAY-2000 (TYEMBL: DT 01-JUN-2001 (TYEMBL: DE KX antigen (1810038 GN XKH OR XK OR 1810038	Eukaryota; Mei Mammalia; Eutl NCBI_TaxID=10	RA L1) RP SEQUENCE FROM N.A. RC STRAIN=BALB/C; TISSI RX MEDLINE=20005522; P.		<pre>KI "Structure and expre RL Immunogenetics 50:16 RN [2]</pre>	RP SEQUENCE FROM N.A. RC STRAIN=BALB/C; TISSI RA Le Van Kim C., Collé RL Submitted (JIN-1999)			RA Arakawa T., Hara A., RA Aizawa K., Izawa M., RA Saito T., Okazaki Y.		RA Schriml L.M., Staubl RA Sakai K., Okido T.,
5.1.4 <u>p5</u> 4578 Compugen_Ltd.		Search time 90 Seconds (without alignments) 1027.946 Million cell updates/sec	RTRVENSEPPFETEARQSVV 449			ters: 671580				•			results predicted by chance to have a . to the score of the result being printed, of the total score distribution.		Description	Q9qxy7 mus musculu Q9h6d3 homo sapien O96pz8 homo sapien	Q8tbaO homo sapien Q8r118 mus musculu O17386 caenorhabdi	Q9v2c2 pyrococcus O48539 oryza sativ	Q942c7 oryza sativ Q9nug5 homo sapien Q9sak8 arabidopsis	Q98qc2 mycoplasma Q9b8z8 schistosoma Q9sa37 arabidopsis	Q94ux1 schistosoma Q94ux2 schistosoma
GenCore version E Copyright (c) 1993 - 2003 (ein - protein search, using sw mode	Run on: April 1, 2003, 08:45:46 ; Se (w	Title: US-09-768-781-3 Perfect score: 2316 Sequence: 1 MDRVYEIPEEPNVDPVSSLE	table: BLOSUM62 Gapop 10.0 , Gapext 0.9	Searched: 671580 seqs, 206047115 residues	Total number of hits satisfying chosen parameters:	Minimum DB seg length: 0 Maximum DB seg length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries		4: sp_numan: 5: sp_invertebrate:* 6: sp_mammal:* 7: sp_mhc:* 8: sp_oranelle:*			Pred. No. is the number of results prediscore greater than or equal to the score and is derived by analysis of the total	SUMMARIES	Result Query No. Score Match Length DB ID	939.5 152 141.5	138.5 6.0 362 4 130 5.6 362 11 129 5.6 439 5	119.5 5.2 382 17	119:5 5:2 943 10 119 5:1 223 4 Q 118:5 5:1 783 10	.9 508 16 .9 424 8 .9 785 10	111.5 4.8 109.5 4.7

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16 Q94UX6 2 Q06039 2 Q06039 5 Q063L7 8 Q04UX8 8 Q011706 8 Q011706 8 Q011707 16 Q08EX39 16 Q08EX39 8 Q011708 8 Q011708 9 Q011708	17 Q9UZC2 16 Q8RB91 10 Q9C8A6 5 Q45426 5 Q8RJ11 16 Q8RN35
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DNA Res. 8:179-187(2001).
EMBL; A8067476; BAB67782.1; -.
NON TER.
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          Submitted (AUG-2001)
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                                         SEQUENCE FROM N.A
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Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                           63 SRDRPLALLAMHLLQLGPLYRCCEVFCIYC---QSDQNEEPYVSITKKRQMPKDGLSEEVE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 KEVGQAEGKLITHRSAPSRASVIQAFLGSAPQLTLQLYITVLEQNITTGRCFIMTLSLLS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 VILVNPFSFPLYPMIVFWCSGSPPPENIEKALSRVGTTIVLCFLTLLYAGINMFCWSAVQ 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 VTYGATLCNMIAIQIKYDDYKIRLGPLEVLCITIWRTLEITSRLLILVLFSATLKLKAVP 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391
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                                                                                                                                                                                                                                                                                                                                                           Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts B.
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., F.
Sasaki H., Satoc K., Schoenbach C., Seya T., Shibate Y., Storch K.-F.
Suzuki H., Toyo-oka K., Wanng K.H., Weitz C., Whittaker C., Wilming L.
Wynnblaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                        33 PPPSILFSTFLYCGEAASALYMVRIYRKNSETYRMTYTFSFFMPSSIMVQLTLIFVHRDL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 FLVLNFLIILFEPWIKFWRSGAQMPNNIEKNFSRVGTLVVLISVTILYAGINFSCWSALQ
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300 LKIDNPELISKSQNWYRLLIYYMTRFIENSVLLLLWYFFKTDIYMYVCAPLLILQLLIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2002 (TrEMBLrel. 21, Last amnotation update)
01-UNN-2002 (TrEMBLrel. 21, Last amnotation update)
CDNA: FLJ22371 fis, clone HRC06680 (Hypothetical 44.7 kDa protein)
(Similar to hypothetical protein FLJ10307).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL: ARTISS11; ARTIS211; ARTIS211; ARTIS2122.1; -.
                                                                                                                                                                                                                                                                      40.6%; Score 939.5; DB 11; Length 446; ilarity 43.8%; Pred. No. 4.7e-70; Conservative 85; Mismatches 135; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 CTGILPMLVFYQFFHPCKKLFSSSVSESFRALLRCACWSS---LRRKSSEP 407
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                                                                                                                                                                                                                                       446 AA; 51114 MW; D785FB7B9E28B98B CRC64;
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SEQUENCE 446 AA; 5
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TISSUE=SKIN;
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                                                                                                                                        Hayashizaki Y.;
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Matches 180;
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MEDLINE=21456161; PubMed=11572484; Magase T, Kikuno R., Ohara O.; Prediction of the coding sequences of unidentified human genes. XXI. "Prediction of the coding sequences of unidentified human genes. The complete sequences of 60 new cDNA clones from brain which code for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 -----SEFDLAYA-DFLALD---ISMLRLFETFLETAPQLTLVLAIMLQS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 AEVPLGRVVLMVFSLVSVTYGATLCNMLAIQIKYDDY------KIRLGPLEVLCIT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 IWRTLEITSRLLILVLFSATL-KLKAVPFLVLNFLIILFEPWIKFWRSGAQ-MPNNIEKN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 FSRVGTLVVLISVTILYAGINFSCWSALOLRLADRDLVDKGONWGHMGLHYSVRLVENVI 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 LYRVTV-----ATILY----FSWFN------VAEGRTRGRAIIHFAFLLSDSIL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363 MVLVFKFFGVKVLLNYCHSLIALQLII-----AYLISIDFMLLFFQYLHPLRSLFTHNVV 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 MFSSIMVQLTLIFVHRDLAKDKPLSLFMHLILLGPVIRCLEAMIKYLTLWKKEEQEEPYV 134
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 21.1%; Pred, No. 0.00012;
Annaervative 71; Mismatches 136; Indels 100;
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Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO26024; BAB15326.1; --
EMBL; BC012379; AAH12379.1; --
EMBL; BC028564; AAH28564.1; --
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                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 395 AA, 44654 MW, 23199BAEEA6964C6 CRC64;
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Waterston R.,
"Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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   01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, Similar to KIAA1889 protein.
                                                                                                                                                                                                                                                         58; Conservative
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                                                    Mus musculus (Mouse)
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                                                                                                                       SEQUENCE FROM N.A.
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                                                                                             NCBI_TaxID=10090;
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                                                                                                                                       TISSUE=COLON;
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                                                                                    158 IRTLAMHRNAYKRMSQIQAFLGSVPQLTYQLYVSLISAEVPLGRVVLMVFSLVSVTYGAT 217
                                                                                                        154 YADVSM------LHLLATFLESAPQLVLQLCIIVQTHSLQALQGFTAAASLVSLAM-AL 205
                                                                                                                                                                   275 INFLILLFEPWIKFWRSGAQMPNNIEKNF--SRVGTLVVLISVTILYAGINFSCWSALQL 332
                                                                                                                                                                                                                               303 ------VKBGRTRCRLFIYYFVILLENTALSALWYLYKAPQIAD-AFAIPALCVVFSSF 354
                             98 LSLFMHLILLGPVIRCLEAMIKYLTLWKKEEQEEPYVSLTRKKWLIDGEEVLIEWEVGHS 157
                                               333 RLADRDLVDKGQNWGHMGLHYSVRLVENVIMVLVPKFPGVKVLLLNYCHSLIALQLII-AY 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 OMPNNIEKOFSRVGTLVVLISVTILYAGINFSCWSALQLRLADRDLVDKGONWGHMGLHY 353
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    61; Gaps
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                                                                                                                                               218 LCNMLAIQIKYDDYKIRLGPLEVLCITI---WRTLEITSRLLILVLFSATLKLKAVPFLV
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
 69; Mismatches 121; Indels
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Strausberg R.;
Strausberg R.;
Submitred (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024146; AAH24146.1; --
SEQUENCE 362 AA; 41672 MW; C19D2D71A2377610 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.0%; Score 138.5; DB 424.7%; Pred. No. 0.0014;
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01-JUN-2002 (TrEMBLrel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similar to KIAA1889 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                               355 LTGVVFMLMYYAPFHP 370
                                                                                                                                                                                                                                                                                                                            392 LISIDEMLLFPQYLHP 407
65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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RESULT 5 QBR118

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130 CMSKWEEILFNMV------VGIVY----IFCWFN------VKEGRIRYRMFAYY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 IQAFLGSVPQLTYQLYVSLISAEVPLGRVVLMVFSLVSVTYGATLCNMLAIQIKYDDYKI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 RIGPLEVLCITIWRTLEITSRLLILVLFSATLKLKAVPFLVLNFLIILFEPWIKFWRSGA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 SMSYRGALIHLFWRLFTISSRVISFALFASIFQLYFGIFVVVHWCAMAF--WIIHGGTDF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 LETFLESAPÓLVLÓLCIMIOKNSAETLPCVSSVTSLMSLAWVLASYHKL-LRDSRDDKK- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 TIVLTENAALTFLWYFYRNPESTDSYAVPALC--C-----VFVSFVAGITLMLLYYGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 OMPINIEKNFSRVGTLVVLISVTILYAGINFSCWSALQLRLADRDLVDKGQNWGHMGLHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 SVRLVENVIMVLVFKF-----FGVKVLLNYCHSLIALQLIIAYLISIDFMLLFFQY
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                        Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                        5.6%; Score 130; DB 11; Length 36
23.8%; Pred. No. 0.0071;
Live 42; Mismatches 100; Indels
                                                                                                                                                                                                               Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024502; AAH24502.1; -. SEQUENCE 362 AA; 41643 MW; 51D0F86C5E548017 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The sequence of C. elegans cosmid F08F1.", Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 51.1 kDa protein.
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240 VLCITIWRTLEITSRLLILVLFSA----
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                                                                                                                                                               155 GHSIRTLAMHRNAYKRMSQ------1QAFLGSVPQL------184
                                                                                                                                                                                     167 ------RKCFSKMVEAERDATLLRFFEAFLESAPQLIIQGSIAASYFQNYYQTGTY 216
                                                                                                                                                                                                                185 TYQLYVSLISAEVPLGRVVLMVFSLVSVTYGATLCNMLAIQIKYDDYKIRLGPLEVLCIT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVIGN-YVYAQMABLTLKEQMM----VASIFYLLTALSMFLAYYLLFNYVTPKRKGGNVE 198
                                                                                                                                                                                                                                  217 PYWLYPQAAS------LLLSIISISWSVVVQNRSLRMIR--DDKVNIWPHEAVLQF 264
                                                                                                                                                                                                                                                                      245 IWRTLEITSRLLILVLFSATLKLKAVPFLVLNPLILLFEPWIKFWRSGAQMPNNJEKNFS 304
                                                                                                                                                                                                                                                                                                  265 CWRFLTILARIITLVA------LVLIF-----GINVAIHIDA-CT 297
                                                                                                                                                                                                                                                                                                                              RVGTLVVLISVTILYAGINPSCWSALQLRLADRDLVDKGQNWGHMGLHYSVRLVENVIMV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrococcus abyssi.
Archaea, Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 QEEPYVSLTRKKMLIDGEEVL----IEWEVGHSIRTLAMHRNAYKRMSQIQAFLGSVP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 QLTYQLYVSLISAKVPLGRVVLMVFSLVSVTYGATLCNMLA---IQIKYDDYKIRLGPLE 239
                                                                                                          97 PLSLPMHLIL--LGPVIRCLEAMIKYLTLWKKEEQEEPYVSLTRKKMLIDGEEVLIEWEV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 SFFM---FSSIMVQLTLIFVHRDLAKDKPLSLFMHLILLGPVIRCLEAMIKYLTLWKKKE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 HIEKLLLLIN-TFIHIFIPF------NWVEGNTRWRYL-TAYSVEFIE---MM
                                                                                                                                   126 PLSKMIVLCICQMGPLFWYYKALY-YGWMPRKSSNEN------TDGEK-----
                                                                                 98; Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.2%; Score 120.5; DB 17; Length 382; Best Local Similarity 22.7%; Pred. No. 0.046; Matches 83; Conservative 56; Mismatches 151; Indels 75;
                                                     Query Match 5.6%; Score 129; DB 5; Length 439; Best Local Similarity 19.4%; Pred. No. 0.011; Matches 67; Conservative 62; Mismatches 98; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Pyrococcus abyssi genome sequence: insights into archaeal structure and evolution.";
Submitted (UTL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ248283; CAB49076.1;
Hypotherical protein; Complete proteome.
SEQUENCE 382 AA; 41459 MW; 08FBA399DAC5AESC CRC64;
EMBL; AF026213; AAB71305.1; -.
Hypothetical protein.
SEQUENCE 439 AA; 51150 MW; E42AC8F17CD2877E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  LVPKFFGVKVLLNYCHSLIALQLIIAYLISIDFMLLFFQYLHPLR 409
                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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18;
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                                                                                                                                                                                                                                 336 DRDLVDKGONWGHMGLHYSVRLVENVIMVLVFKFFGVKVLLNYCHSLIALQLIIAYLISI 395
                                                                                                                                                                                                                                                                  98 LSLFWHLILLGPVIRCLEAMIKYL-----TLWKKBEQEEPYVSLTRKKMLIDGEEVL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 MVFSLVSVTYGATLCNMLAIQIKYDDYKIRLGPLEVLCITI-----WRTLEITSRLLIL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 ----TSLSY------YFEDNWKRLWVL-ALWIGIMAGLFTWKFMQYRNRYVFD 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 VL-FSATLKLKAVPFLVLNFLIILFE-----PWIKFWRSGAQMPNNIEKNFSRVGTLVV 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 VMGYCVTTAKGAAETLKLNMAIILLPVCRNTITWLRSTRAARALPFDDNINPHKTIAAAI 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 LISVTILYAGINFSCWSALQLRLADRDLVDKGQNWGHMGLHY-----SVRLVENVIMVLV 366
-----TLKLKAVPFLVLNFLIIL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 STFLYC-GEAASALYMVRIYRKNSETYRMTY-TFSFFMFSSIMVQLTLIFVHRDLAKDKP 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 SDFAECIGMTESKEFALELFDTLSRRRQMKVDTINKDELREIWQQIT-----DNSFDSR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keller T., Damude H.G., Werner D., Doerner P., Dixon R.A., Lamb C., "A plant homolog of the neutrophil NADPH oxidase gp91phox subunit gencedes an intrinsic plasma membrane protein with Ca2+-binding and RandApl domains "; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AFOL3302, AAB87790.1; -InterPro; IPR002048; EF-hand. InterPro; IPR002048; EF-hand. InterPro; IPR000578; GP91PhoX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, Lillopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza, WCBI_TaxID=4530;
                                    282 FEPWIKFWRSGAQMPNNIEKNFSRVGTLVVLIS-----VTILYAGINFSCWSALQLR-LA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                745 AA; 85335 MW; 8734D3E13A46B3B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Pfam, PF00005; effand, 1.
Pfam, PF01794; Perric reduct; 1.
PRINTS; PR00466; GP91PHOX.
PROSITE; PS00018; EF_HAND; UNKNOWN_1.
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89; Conservative
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01-JUN-1998 (TrEMBLrel.
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Keller T., Damude
                                                                                                                                                                                                                                                                                                                                                396 DFMLL 400
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471 VVGI-ILHAGNHLVCDFPRLIKSSDBKYAPLGQYFGBIKPTYFTLVKGVEGITGVIMVVC 529
                                   312 LISVTILYAGINFSCWSALQLRLADRDLVDKGQNWGHMGLHY----SVRLVENVIMVLV 366
                                                                                                                                                                530 MIJAFTLATRWFRRSLVKLPRPFDKLTGFNAFW-YSHHLFIIVYIALIVHGECLYLIHVW 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 IQAFLGSVPQLTYQLYVSLISAEVP-LGRVVLMVFSLVSVTYGATLCNMLAIQIKYDDYK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 IRLGPLEVLCITIWRTLEITSRLLILVLFSATLKLKAVPFLVLNFLILFEPWIKFWRSG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 AQMPINIEKNFSRVGTLVVLISVTILYAGINFSCWSALQLRLADRDLVDKGQNWGHMGLH 352
                                                                                                                        -----KFFGVKVLLNYCHSL---IALQLII----AYLISID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 --IQGETDFCMSKWEEIIYNMVVGIIY----IFCWFN------VKEGRSRRRTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9NUG5;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OUN-2002 (TrEMBLrel. 21, Last annotation update)
DJ310013.4 (Novel protein similar to predicted C. elegans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 YSVRLVENVIMVLVFKFFGVKVLLNYCHSLIALQLII-AYLISIDFMLLFFQYLHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.1%; Score 119; DB 4; Length 223; 22.9%; Pred. No. 0.035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kay M.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, AL031658; CAB88102.1; -.
InterPro; IPR00504; RNA rec mot.
PROSITE; PS00030; RRM RNP 1; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 AA; 25490 MW; 78A0554C03B9F70D CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                           223
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                                                                                                                      367 F----
                                                                                                                                                                                                       397 FMLLFFQYL 405
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Q9SAK8;
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Matches
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273 VVGI-ILHAGNHLVCDFPRLIKSSDEKYAPLGQYFGBIKPTYFTLVKGVEGITGVIMVVC 331
                                                                 367 F----AYLISID 396
                                                                                                           332 MIJAPTLATRWFRRSLVKLPRPFDKLTGFNAFW-YSHHLFIIVYIALIVHGECLYLIHVW 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 LSLFMHLILLGPVIRCLEAMIKYL-----TLWKKEEQEEPYVSLTRKKMLIDGEEVL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 SDFAECIGMTESKEFALELFDTLSRRRQMKVDTINKDELREIWQQIT-----DNSFDSR 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |: :||:::|| || || 323 ELWQ----LETLLLLQKOTYMNYSQALSYTSQALSQNLAGLRKKKSSIRKIS------ 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 -----TSLSY------YPEDNWKRLWVL-ALWIGIMAGLFTWKFMQYRNRYVFD 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice), and oryza sativa (Japonica cultivar-group).

Gryza sativa (Japonica cultivar-group).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Brhartcideae; Oryzaee;

Oryzae, Oryzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 IEWEVGHSIRTLAMHRNAYKRMSQI-----QAFLGSVPQLTYQLYVSLISAEVPLGRVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 UL-PSATLKLKAVPPLVLNFLIILFE-----PWIKFWRSGAOMPNNIEKNFSRVGTLVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5:2%; Score 119.5; DB 10; Length 943; Best Local Similarity 20.7%; Pred. No. 0.14; Matches 89; Conservative 66; Mismatches 171; Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
STRAIN=CV. NIPPONBARE;
SABAKI T., MATSUMOTO T., YAMAMOTO K.;
GOTYZA SELIVA ALEDONDATE (GA3) GENOMIC DNA, Chromosome 1, BAC clone:OSJNBb0036G99.";
SUDMITTER (GAS) CO. THE EMBL/GenBank/DDBJ databases.
EMBL; AP003309; BAB89942.1; ---
EMBL; AP003309; BAB89942.1; ---
EMBL; AP003309; BAB89942.1; ---
InterPro; IPR002916; Ferric_reduct.
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STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
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Pfam; PF01794; Ferric_reduct; 1.
PROSITE; PS00018; BF HAND; UNKNOWN 1.
SEQUENCE 943 AA; 106257 WW; 6B5EDE1339D28657 CRC64;
                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Cytochrome b245 beta chain homolog rbohA.
B106,0H01.12 OR OSJNBB0036G99.18
                                                                                                                                                                                                                                                                                                          943 AA
                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                     397 PMLLPFQYL 405
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complete genome sequence of the murine respiratory pathogen
                                                                                                                                                                                                                         4.9%; Score 113.5; DI 18.3%; Pred. No. 0.24;
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Interpro; IPR003918; NADHub oxred4.
Interpro; IPR001750; Oxidored_q1.
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Schistosoma japonicum (Blood fluke)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453 KSLSTLKTEKKPWTFNKKNIFDY 475
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                                                                                                                                                                                                                                                                              81; Conservative
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                                                                                                                                                                                                                                                  Similarity
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Q9B8Z8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 FFMFSSIMVQLTLIFVHRDL-----AKDKPLSLFMHLILLGPVIRCLEAMIKYLTLW 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 KKEEQEEPYVS--LTRKKMLIDGEEVLIEWEVGHSIRTLAMHRNAYKRMSQI--QAFL-- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 KNAADYYSPPSFALRTSPMFLIGLEVDLHF------MRRN-FKKAAVITLSSFVVS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 GSVPQLTYQLYVSLISAEVPLGRVVLAVFSLVSVTYGATLCNMLAIQIKYDDYKI---RL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : | : | : | : | : | : | 1.25 GLLSFASIMLFIPLFGIKEDYFTFFLVLLVTLSNTASPVVVRSIA-----DWKLNTCEI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 GPLEVLCITIWRTLEITSRLLILVLFSATLKLKAVPFLVLNFLILLFE----PWIKFWRS 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 GRLTISCALFIELTNVVLYTIİMAFISGTIILELFLELATVALILINMVLAPWL---- 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 GAQMPNNIEKNPSRVGTLVVLI------SVTILYAGINFSCWSALQLRLA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 -- PKRNPKEKYLSKARTLVFFIFLLIIGITIESYDVNSSVSVFAIGIMFP-----RQGKT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336 DRDLVDK-----GONWGHMGLHYSV-----RLVENVIMVLVPKPFGV---- 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 HRTLIQRLSYPIHEFVLPVYFGYIGFRFSIIALTKRFYLGIVIIVIVTJAGKFIGVISAC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 MYLKIPKKYWLFLPTILSVKGHVGLLILDSNYSEKKWWTTTTHDMMVAALVITTLVSGVL 406
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.1%; Score 118.5; DB 10; Length 783; Best Local Similarity 19.6%; Pred. No. 0.14; Matches 89; Conservative 69; Mismatches 166; Indels 129; Gaps
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                                                                        STRAIN-CY. COLUMBIA,
Vysotekaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Li J., Kremenetekaia I., Luros J., Lee J.M., Gonzalez A., Altafi H.,
Araujo R., Chao O., Conn L., Conway A.B., Dunn P., Hansen N.,
Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
Bavis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ACOTOSO, AAD30236.1;
Interpro, IPR000676, NaH Exchngr.
Effam, PR009999, Na H Exchanger;
SEQUENCE 783 AA; B8203 MW, OA6846910C381648 CRC64;
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Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha B.P.C.,
Blanchard A.;
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01-OCT-2001 (TrEWBLrel. 18, Created)
01-OCT-2001 (TrEWBLrel. 18, Last sequence update)
01-OCT-2001 (TrEWBLrel. 18, Last annotation update)
Hypothetical protein MYPU_4440.
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NCBI_TaxID=2107;
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                                                       SEQUENCE FROM N.A
  WCBI_TaxID=3702;
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Le T.H., Blair D., Agatsuma T., Humair P.F., Campbell N.J., Invagami M., Littlewood D.T., Peacock B., Johnston D.A., Bartley J., Rollinson D., Herniou E.A., Zarlenga D.S., McManus D.P., "Phylogenies inferred from mitochondrial gene orders-a cautionary tale
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Schistosomatoidea, Schistosomatidae, Schistosoma.
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Mol. Biol. Evol. 17:1123-1125(2000).
-!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
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Mycoplasma pulmonis.";
Nucleic Acids Res 29:2145-2153(2001).
EMBL, AL445564; CAC13617.1; -.
Mypulist; MYPU Totein; Complete proteome.
SRQUENCE 508 AA; 61075 MW; 46E82551297E7642 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3)
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Pfam; PF00999; Na H Exchanger; 1.
SEQUENCE 785 AA; 89908 MW; 3830426AAA66CB1C CRC64;
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Vysotekaia V.S., Schwartz J., Yu G., Toriumi M., Lenz C., Liu S.,
Vysotekaia V.S., Schwartz J., Yu G., Toriumi M., Lenz C., Liu S.,
Lee J., Li J., Kremenetskaia I., Liu A., Luros J., Gonzalez R.,
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Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"The sequence of BAC Floyd From Arabidopsis thaliana chromosome 1.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                    DLAKDKPLSLFMHLILLGPVIRCLEAMIKY-----LTLWKKEEQEEPYVSLTRKKMLIDG 145
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
Pfam; PF00361; Oxidored q1; 1.
PRINTS; PR01437; NUOXDRDTASE4.
Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SRQUENCE 424 AA; 47741 MW; 377C53E611F57D72 CRC64;
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Last annotation update)
                                                                                                                                                           Query Match 4.9%; Score 112.5; DB 8; Best Local Similarity 19.5%; Pred. No. 0.24; Matches 90; Conservative 77; Mismatches 156;
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InterPro; IPR000676; NaH Exchngr
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01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
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MEDLINE=20349913; PubMed=10889225;
Lef T.H., Blair D., Agatsuma T., Humair P.F., Campbell N.J.,
Lef T.H., Blair D., Peacock B., Johnston D.A., Bartley J.,
Rollinson D., Herniou E.A., Zarlenga D.S., McManus D.P.;
"Phylogenies inferred from mitochondrial gene orders-a cautionary tale
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 FRFS----VNSLTKKHYLVLGMTVALSLLGKLLGVLFACSFLKIPKOYWLFLSTMLSVK- 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365 -----GHIGL---VLLDSN----LMYKKWFTPVV----HDMFVAALVIMTLLEGGVIT 405
                                                                                                                                                                                   84 TLIF-VHRDLAKDKPLSLFMHLILLGPVIRCLEAMIKYLTLWKKEEQEEPYVSLTRKKML 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 -VLCITIWRTLE---ITSRLLIIV---LFSATLK-----LKAVPFLVLNFLIILFEPWIK 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 LVDKGQNWGHMGLHYSVRLVENVIMVLVFKFFGVKVLLNYCHSLIALQLIIAYLIS--ID 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                  Gape
                                                                                                                          30 LVFSQFFYLFLKPCGQAGPVAQILAGIVLSLLTIIRKVHEFFLQKDSASYYIFFSFLRRT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Le T.H., Blair D., McManus D.P., _{\rm I} "Revisiting limited genetic variation within Schistosoma japonicum
                                                                                        37 ILFSTFLY-----CGEAAS------ALYMVRIYRKNSETYRMTYTFSFFMFSSIMVQL
                                                                                                                                                                                                                               90 AFVFLIGLEIDLD-----FMKRNLKNSIVITLGSLVISGIIWL-----PFLWFLIRFMQ
                                                                                                                                                                                                                                                                                                                                                                     181 VPQLTYQLYVSLISAEVPLGRVVLMVFSLVSVTYGATLCNMLAIQIKYDDYKIRLGPLE-
  Length 785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 populations.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DB 10;
4.9%; Score 112.5; DB 10;
19.7%; Pred. No. 0.45;
iive 84; Mismatches 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             406 SLLLRSOEKSFAHIKTSLELFDTTEELRVLTC 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 FMLLFFQ---YLHPLRSLFTHNVVDYLHCVCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schistosoma japonicum (Blood fluke).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Biol. Evol. 17:1123-1125(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AF412213; AAL12155.1; -. InterPro; IPR001750; Oxidored_q1. Pfam; PF00361; oxidored_q1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NADH dehydrogenase subunit
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                     Local Similarity
es 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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20;
                                                                                                                                                                                                                                                                                                                           91 DLAKDKPLSLFMHLILLGPVIRCLEAMIKY-----LTLWKKEEQEEPYVSLTRKKMLIDG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 VGLVRLCGWLJID-----YIYYFSTFLLCYSVVFLV----AAVFECDSKRWLAYLSLSH 266
                                                                                                                                                                                                                                                                                                                                                                                   71 WLVGSKDIVLF-----ISVFSAMLTYVVSNSLVFWFFYELS----IISALYMLIVG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 SPYPERYISSWYPGGYI------1LLSSVPLLLGICFIGLNSGSF---N 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 VVLMVPSLVSVTYGATLCNML-------A1QIKYDDYKIRLGP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 LEVLCITIWRTLEITSRLLILVLPSATLKLKAVPFLVLNFLILLFEPWIKFWRSGAQMPN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 NIEKNFSRVGTLVVL------ISVTILYAGINFSCWSALQLRLADRDL 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : :| ::| : | 308 267 IL------IGVCILLTSTYCGDYLAFIYCLGHGLSVALLFMII-----WFGYE------ 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 VDKGQNWGHMGLHYSVRLVENVIMVLVF------KRFG-VKVLLNY--CHSLIALQ 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 ISGSRNWGILUXKIFGGGLIMHFIMGFVFLNVCGFPPALQFFGELWLVINYITLGDIISLL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 ----EEVLIEWEVGHSIRTLAMHRNAYKRMSQIQAFLGSVPQLTYQLYVSLISAEVPLGR 201
                                                                                 Query Match

4.8%; Score 111.5; DB 8; Length 424;
Best Local Similarity 19.5%; Pred. No. 0.29;
Matches 90; Conservative 77; Mismatches 156; Indels 139; Gaps
                                                                                                                                                                                                                                                18 TPIFLLIPYSSIWVSDSSWWWGVKYYLCDGLVIIDT-----LSCLMIFLTSIMLVL 70
                                                                                                                                                                                                       32 TPPFSILPSTFLYCGEAASALYMVRIYRKNSETYRWTYTFSFFMFSSIMVQLT-LIFVHR 90
Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SEQUENCE 424 AA; 47725 MW; 1BC880B001235E31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387 LIIAYLIS---IDFMLLFPQYLHPLRSLFTHN--VVDYLHCV 423
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Search completed: April 1, 2003, 08:50:40 Job time: 96 secs

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